



THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Marc Albertsen et al.	1	Art Unit: 1638
Serial No.: 10/021,657	1	
Filed: December 14, 2001	1	Examiner: A. Kubelik
For: Nucleotide Sequences Mediating Fertility and Method of Using Same	1	Confirmation No. 5787

DECLARATION UNDER 37 CFR §1.131

Commissioner for Patents
Washington, D.C. 20231
Sir:

I, Tim Fox, declare and say:

I am an inventor for the above-identified application. I conceived and reduced to practice in the United States the invention claimed in the above-identified patent application prior to February, 2000, the publishing date of the reference to Genbank accession AW424821.2; prior to March, 2000, the publishing date of the reference to Genbank accession AW519943; and prior to August 2000, the publishing date of the reference to Genbank accession BE494080.1. Attached Exhibit A is the sequence of the SBMu200 gene, which sequencing was conducted at my instructions by our contractor and provided to before the dates identified above.

The invention was thus conceived and reduced to practice in the United States prior to February 2000. The Exhibit, which relates to the conception and actual reduction to practice, corresponds to the invention broadly disclosed and claimed in the above-identified application.

The undersigned declares further that all statements made herein of his own knowledge are true and all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful, false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of title 18 United States Code and that such willful false statements may jeopardize the validity of the application or any patents issuing thereon.

10/18/04

Date

Tim Fox

USSN 10/021,657
Exhibit A

(Linear) MAP of: Sb20081.Seq check: 1232 from: 1 to: 1906

REFORMAT of: Sb20081.Seq check: -1 from: 1 to: 1912 10:59
TASSEL SPECIFIC cDNA ISOLATED FROM MAIZE INBRED A632. THIS CLONE IS MISSING
THE FIRST MET, WHICH MAY BE DUE TO CLONING ARTIFACT AS COMPARED TO THE GENOMIC.
cDNA LIBRARY MADE FROM MAIZE TASSEL mRNA IN UNI-ZAP VECTOR (STRATAGENE).
SEQUENCING DONE BY LOFTSTRAND AND IS DOUBLE STRAND VERIFIED.

With 2 enzymes: ECORI XHOI

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EcoRI
|
GAATTCGGGCACGAGGGAAGCTCACCTCACGCCGCGACGCCATCGCCATTCTTCCCACTA
1 -----+-----+-----+-----+-----+-----+ 60
CTTAAGCCGTGCTCCCTTCGAGTGGAGTGCGCCGCTGCGGTAGCGGTAAGAAGGGTGAT

a E F G T R E A H L T P A T P S P F F P L -

GCAGGGCCTCACAAGTACATCGCGCTCCTTCTGGTTGTCCTCTCATGGATCCTGGTCCAG
61 -----+-----+-----+-----+-----+ 120
CGTCCCGGAGTGTTTCATGTAGCGCGAGGAAGACCAACAGGAGAGTACCTAGGACCAGGTC

a A G P H K Y I A L L L V V L S W I L V Q -

AGGTGGAGCCTGAGGAAGCAGAAAGGCCGAGATCATGGCCAGTCATCGGCGCAACGGTG
121 -----+-----+-----+-----+-----+ 180
TCCACCTCGGACTCCTTCGTCTTTCCGGGCTCTAGTACCGGTCAGTAGCCGCGTTGCCAC

a R W S L R K Q K G P R S W P V I G A T V -

GAGCAGCTGAGGAACTACCACCGGATGCACGACTGGCTTGTCGGGTACCTGTACGGCAC
181 -----+-----+-----+-----+-----+ 240
CTCGTCGACTCCTTGATGGTGGCCTACGTGCTGACCGAACAGCCCATGGACAGTGCCGTG

a E Q L R N Y H R M H D W L V G Y L S R H -

AGGACAGTGACCGTCGACATGCCGTTCACTTCCTACACCTACATCGCTGACCCGGTGAAT
241 -----+-----+-----+-----+-----+ 300
TCCTGTCACTGGCAGCTGTACGGCAAGTGAAGGATGTGGATGTAGCGACTGGGCCACTTA

a R T V T V D M P F T S Y T Y I A D P V N -

GTCGAGCATGTCTCAAGACTAACTTCACCAATTACCCCAAGGGAATCGTGTACAGATCC
301 -----+-----+-----+-----+-----+ 360
CAGCTCGTACAGGAGTTCTGATTGAAGTGGTTAATGGGGTTCCCTTAGCACATGTCTAGG

a V E H V L K T N F T N Y P K G I V Y R S -

TACATGGACGTGCTCCTCGGTGACGGCATCTTCAACGCCGACGGCGAGCTGTGGAGGAAG
361 -----+-----+-----+-----+-----+ 420
ATGTACCTGCACGAGGAGCCACTGCCGTAGAAGTTGCGGCTGCCGCTCGACACCTCCTTC

a Y M D V L L G D G I F N A D G E L W R K -

CAGAGGAAGACGGCGAGTTTCGAGTTCGCCTCCAAGAACCTGAGGGATTTACAGCGCCATT
421 -----+-----+-----+-----+-----+ 480
GTCTCCTTCTGCCGCTCAAAGCTCAAGCGGAGGTTCTTGACTCCCTAAAGTCGCGGTAA

a Q R K T A S F E F A S K N L R D F S A I -

481 GTGTTTCAGAGAGTACTCCCTGAAGCTGTCGGGTATACTGAGCCAGGCATCCAAGGCAGGC
 -----+-----+-----+-----+-----+-----+-----+ 540
 CACAAGTCTCTCATGAGGGACTTCGACAGCCCATATGACTCGGTCCGTAGGTTCCGTCCG
 a V F R E Y S L K L S G I L S Q A S K A G -
 AAAGTTGTGGACATGCAGGAACTTTACATGAGGATGACGCTGGACTCCATCTGCAAGGTT
 541 -----+-----+-----+-----+-----+-----+ 600
 TTTCAACACCTGTACGTCTTGAAATGTACTCCTACTGCGACCTGAGGTAGACGTTCCAA
 a K V V D M Q E L Y M R M T L D S I C K V -
 GGGTTCGGGGTCGAGATCGGCACGCTGTCGCCAGATCTCCCCGAGAACAGCTTCGCGCAG
 601 -----+-----+-----+-----+-----+-----+ 660
 CCCAAGCCCCAGCTCTAGCCGTGCGACAGCGGTCTAGAGGGGCTCTTGTCGAAGCGCGTC
 a G F G V E I G T L S P D L P E N S F A Q -
 GCGTTCGATGCCGCCAACATCATCATCACGCTGCGGTTTCATCGACCCGCTGTGGCGCATC
 661 -----+-----+-----+-----+-----+-----+ 720
 CGCAAGCTACGGCGGTTGTAGTAGTAGTGCGACGCCAAGTAGCTGGGCGACACCGCGTAG
 a A F D A A N I I I T L R F I D P L W R I -
 AAGAGTTCTTCCACGTCGGGTCAGAGGCCCTCCTAGCGCAGAGCATCAAGCTCGTGGAC
 721 -----+-----+-----+-----+-----+-----+ 780
 TTCTCCAAGAAGGTGCAGCCCAGTCTCCGGGAGGATCGCGTCTCGTAGTTCGAGCACCTG
 a K R F F H V G S E A L L A Q S I K L V D -
 GAGTTCACCTACAGCGTGATCCGCCGGAGGAAGGCCGAGATCGTCGAGGTCCGGGCCAGC
 781 -----+-----+-----+-----+-----+-----+ 840
 CTCAAGTGGATGTCGCACTAGGCGGCCTCCTTCCGGCTCTAGCAGCTCCAGGCCCGGTG
 a E F T Y S V I R R R K A E I V E V R A S -
 GGCAAACAGGAGAAGATGAAGCACGACATCCTGTCACGGTTCATCGAGCTGGGCGAGGCC
 841 -----+-----+-----+-----+-----+-----+ 900
 CCGTTTGTCTCTTCTACTTCGTGCTGTAGGACAGTGCCAAGTAGCTCGACCCGCTCCGG
 a G K Q E K M K H D I L S R F I E L G E A -
 GGCGACGACGGCGGCGGCTTCGGGGACGATAAGAGCCTCCGGGACGTGGTGCTCAACTTC
 901 -----+-----+-----+-----+-----+-----+ 960
 CCGCTGCTGCCGCCGCCGAAGCCCCTGCTATTCTCGGAGGCCCTGCACCACGAGTTGAAG
 a G D D G G G F G D D K S L R D V V L N F -
 GTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTCGTGGTTCACGCACATGGCCATG
 961 -----+-----+-----+-----+-----+-----+ 1020
 CACTAGCGGCCCCGCCCTGTGCTGCCGCTGTGCGACAGCACCAAGTGCGTGTACCGGTAC
 a V I A G R D T T A T T L S W F T H M A M -
 TCCCACCCGACGTGGCCGAGAAGCTGCGCCGCGAGCTGTGCGCGTTCGAGGCGGAGCGC
 1021 -----+-----+-----+-----+-----+-----+ 1080
 AGGGTGGGCCTGCACCGGCTCTTCGACGCGGCGCTCGACACGCGCAAGCTCCGCCTCGCG
 a S H P D V A E K L R R E L C A F E A E R -

1081 GCGCGCGAGGAGGGCGTCACGCTCGTGCTCTGCGGCGGCGCTGACGCCGACGACAAGGCG
 -----+-----+-----+-----+-----+-----+ 1140
 CGCGCGCTCCTCCCGCAGTGCGAGCACGAGACGCCGCCGCGACTGCGGCTGCTGTTCCGC

 a A R E E G V T L V L C G G A D A D D K A -

 1141 TTCGCCGCCCCGCGTGGCGCAGTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTG
 -----+-----+-----+-----+-----+-----+ 1200
 AAGCGGCGGGCGCACCGCGTCAAGCGCCCCGAGGAGTGGATGCTGTGCGGAGCCGTTTCGAC

 a F A A R V A Q F A G L L T Y D S L G K L -

 1201 GTCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTCCCTCAGGAC
 -----+-----+-----+-----+-----+-----+ 1260
 CAGATGGAGGTGCGGACGCAGTGGCTCTGCGAGGCGGACATGGGGCGGCAGGGAGTCCTG

 a V Y L H A C V T E T L R L Y P A V P Q D -

 1261 CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAGGGCCGGCGGG
 -----+-----+-----+-----+-----+-----+ 1320
 GGGTTCCTTAGGACCTCCTGCTGCACGACGGCTGCCCTGCTTCCACTCCCGGCCGCC

 a P K G I L E D D V L P D G T K V R A G G -

 1321 ATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGTACAACCTGGGGCCCCGACGCG
 -----+-----+-----+-----+-----+-----+ 1380
 TACCACTGCATGCACGGGATGAGCTACCCGCTACCTCATGTTGACCCCGGGGCTGCGC

 a M V T Y V P Y S M G R M E Y N W G P D A -

 1381 GCGAGCTTCCGGCCGAGCGGTGGATCAACGAGGATGGCGCGTTCCGCAACGCGTCGCCC
 -----+-----+-----+-----+-----+-----+ 1440
 CGCTCGAAGGCCGGCCTCGCCACCTAGTTGCTCCTACCGCGCAAGGCGTTGCGCAGCGGC

 a A S F R P E R W I N E D G A F R N A S P -

 1441 TTCAAGTTCACGGCGTTCAGGCGGGGCCGAGGATCTGCCTGGGCAAGGACTCGGCGTAC
 -----+-----+-----+-----+-----+-----+ 1500
 AAGTTCAAGTGCCGCAAGGTCCGCCCCGGCTCCTAGACGACCCGTTCTGAGCCGCATG

 a F K F T A F Q A G P R I C L G K D S A Y -

 1501 CTGCAGATGAAGATGGCGCTGGCCATCCTCTTCCGCTTCTACAGCTTCCGGCTGCTGGAG
 -----+-----+-----+-----+-----+-----+ 1560
 GACGTCTACTTCTACCGCGACCGGTAGGAGAAGGCGAAGATGTCTGAAGGCCGACGACCTC

 a L Q M K M A L A I L F R F Y S F R L L E -

 1561 GGGCACCCGGTGCAGTACCGCATGATGACCATCCTCTCCATGGCGCACGGCCTCAAGGTC
 -----+-----+-----+-----+-----+-----+ 1620
 CCCGTGGGCCACGTCATGGCGTACTACTGGTAGGAGAGGTACCGCGTGCCGGAGTTCAG

 a G H P V Q Y R M M T I L S M A H G L K V -

 1621 CGCGTCTCTAGGGCCGTCTGATGTCATGGCGATTTGGATATGGATATCGTCCCGCTTAAT
 -----+-----+-----+-----+-----+-----+ 1680
 GCGCAGAGATCCCGGCAGACTACAGTACCGCTAAACCTATACCTATAGCAGGGCGAATTA

 a R V S R A V * C H G D L D M D I V P L N -

 CCACGACAAATAACGCTCGTGTTACAAATTTGCATGCATGCATGTAAGGGAAAGCGATGG

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1681 -----+-----+-----+-----+-----+ 1740
      GGTGCTGTTTATTGCGAGCACAAATGTTTAAACGTACGTACGTACATTCCCTTTCGCTACC
a      P R Q I T L V L Q I C M H A C K G K R W -
      GTTTCATTGGTGGCTTGGCTTAAGCCTTAAAACTCCGTCGGGTCTTGCGAACCACCACA
1741 -----+-----+-----+-----+-----+ 1800
      CAAAGTAACCACCGAACCGAATTCGGAATTTTGGAGGCAGCCCAGAACGCTTGGTGGTGT
a      V S L V A W L K P *
      TCACTAGTGTTTTGTACTCTACTCCTCAGTGGAAGTGTAGTGACAGCATACAAGTTCATC
1801 -----+-----+-----+-----+-----+ 1860
      AGTGATCACAAAACATGAGATGAGGAGTCACCTTCACATCACTGTCGTATGTTCAAGTAG

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                                     XhoI
                                     |
ATATATATTATCCTCTTTCTTAAAAAAAAAAAAAAAAAACTCGAG
1861 -----+-----+-----+-----+----- 1906
      TATATATAATAGGAGAAAGAATTTTTTTTTTTTTTTTTTTGAGCTC

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